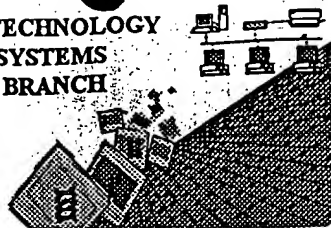


Re-run

BIOTECHNOLOGY
SYSTEMS
BRANCH



S. Brown

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/757,655
Source: /600
Date Processed by STIC: 2/21/2002

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/257,655

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to 3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. "Please" ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
"bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
(OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
(NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
(NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
"bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

Re-run



160

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/757,655

DATE: 02/21/2002
TIME: 11:38:41

Input Set : A:\FUJII SEQUENCE LISTING.txt
Output Set: N:\CRF3\02212002\I757655.raw

Does Not Comply
Corrected Diskette Needed

pg 1-5

3 <110> APPLICANT: FUJII, Takeru
4 YOKOYAMA, Hideakira
5 HAMAMOTO, Hidetoshi
7 <120> TITLE OF INVENTION: A PEPTIDE HAVING AN AFFINITY FOR gp120
9 <130> FILE REFERENCE: 2001-0019A/LC/01732
11 <140> CURRENT APPLICATION NUMBER: 09/757,655
12 <141> CURRENT FILING DATE: 2001-01-11
14 <150> PRIOR APPLICATION NUMBER: JP No. 2000-6182
15 <151> PRIOR FILING DATE: 2000-01-11
17 <160> NUMBER OF SEQ ID NOS: 19
19 <170> SOFTWARE: PatentIn Ver. 2.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 5
23 <212> TYPE: PRT
24 <213> ORGANISM: Artificial Sequence
26 <220> FEATURE:
27 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
29 <220> FEATURE:
W--> 30 <221> NAME/KEY: Residue
31 <222> LOCATION: (1)
32 <223> OTHER INFORMATION: Xaa = Asp, Lys, Val, Glu, Gly, Asn or Tyr
34 <220> FEATURE:
W--> 35 <221> NAME/KEY: Residue
36 <222> LOCATION: (2)
37 <223> OTHER INFORMATION: Xaa = Val, Asp, Trp, Lys, Phe, Ile, Leu or Tyr
39 <220> FEATURE:
W--> 40 <221> NAME/KEY: Residue
41 <222> LOCATION: (3)
42 <223> OTHER INFORMATION: Xaa = Lys, Val, Asp, Arg, Ala or Trp
44 <220> FEATURE:
W--> 45 <221> NAME/KEY: Residue
46 <222> LOCATION: (4)
47 <223> OTHER INFORMATION: Xaa = Ala, Trp or Gly
49 <220> FEATURE:
W--> 50 <221> NAME/KEY: Residue
51 <222> LOCATION: (5)
52 <223> OTHER INFORMATION: Xaa = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, Asn, Gln, His,
Lys, Arg,
53 Phe, Trp, Pro or Tyr
55 <400> SEQUENCE: 1
56 Xaa Xaa Xaa Xaa Xaa
57 1 5
59 <210> SEQ ID NO: 2
60 <211> LENGTH: 5

insufficient explanation
give source
of genetic
material
(see item
on Error
summary
sheet)

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/757,655

DATE: 02/21/2002

TIME: 11:38:41

Input Set: A:\FUJII SEQUENCE LISTING.txt

Output Set: N:\CRF3\02212002\I757655.raw

61 <212> TYPE: PRT
 62 <213> ORGANISM: Artificial Sequence
 64 <220> FEATURE:
 65 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide *same error*
 67 <220> FEATURE:
 W--> 68 <221> NAME/KEY: Residue
 69 <222> LOCATION: (1)
 70 <223> OTHER INFORMATION: Xaa = Asp, Lys, Val, Glu, Gly, Asn or Tyr, or polypeptide residue that an
 71 arbitrary amino acid stood in line in the N-terminal side from this amino acid
 73 <220> FEATURE:
 W--> 74 <221> NAME/KEY: Residue
 75 <222> LOCATION: (2)
 76 <223> OTHER INFORMATION: Xaa = Val, Asp, Trp, Lys, Phe, Ile, Leu or Tyr
 78 <220> FEATURE:
 W--> 79 <221> NAME/KEY: Residue
 80 <222> LOCATION: (3)
 81 <223> OTHER INFORMATION: Xaa = Lys, Val, Asp, Arg, Ala or Trp
 83 <220> FEATURE:
 W--> 84 <221> NAME/KEY: Residue
 85 <222> LOCATION: (4)
 86 <223> OTHER INFORMATION: Xaa = Ala, Trp or Gly
 88 <220> FEATURE:
 W--> 89 <221> NAME/KEY: Residue
 90 <222> LOCATION: (5)
 91 <223> OTHER INFORMATION: Xaa = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, Asn, Gln, His
 Lys, Arg,
 92 Phe, Trp, Pro or Tyr
 94 <400> SEQUENCE: 2
 W--> 95 Xaa Xaa Xaa Xaa Xaa
 96 1 5
 98 <210> SEQ ID NO: 3
 99 <211> LENGTH: 5
 100 <212> TYPE: PRT
 101 <213> ORGANISM: Artificial Sequence
 103 <220> FEATURE:
 104 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
 106 <220> FEATURE:
 W--> 107 <221> NAME/KEY: Residue
 108 <222> LOCATION: (1)
 109 <223> OTHER INFORMATION: Xaa = Asp, Lys, Val, Glu, Gly, Asn or Tyr
 111 <220> FEATURE:
 W--> 112 <221> NAME/KEY: Residue
 113 <222> LOCATION: (2)
 114 <223> OTHER INFORMATION: Xaa = Val, Asp, Trp, Lys, Phe, Ile, Leu or Tyr
 116 <220> FEATURE:
 W--> 117 <221> NAME/KEY: Residue
 118 <222> LOCATION: (3)
 119 <223> OTHER INFORMATION: Xaa = Lys, Val, Asp, Arg, Ala or Trp
 121 <220> FEATURE:
 W--> 122 <221> NAME/KEY: Residue

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/757,655

DATE: 02/21/2002
TIME: 11:38:41

Input Set : A:\FUJII SEQUENCE LISTING.txt
Output Set: N:\CRF3\02212002\I757655.raw

123 <222> LOCATION: (4)
124 <223> OTHER INFORMATION: Xaa = Ala, Trp or Gly
126 <220> FEATURE:
W--> 127 <221> NAME/KEY: Residue
128 <222> LOCATION: (5)
129 <223> OTHER INFORMATION: Xaa = Gly, Ala, Val, Leu, Ile, Thr, Met, Asn, Gln, His, Lys,
Arg,
130 Phe, Trp, Pro or Tyr, or polypeptide residue that an arbitrary amino acid
131 stood in line in the C-terminal side of this amino acid, H
133 <400> SEQUENCE: 3
W--> 134 Xaa Xaa Xaa Xaa Xaa
135 1 5
138 <210> SEQ ID NO: 4
139 <211> LENGTH: 5
140 <212> TYPE: PRT
141 <213> ORGANISM: Artificial Sequence
143 <220> FEATURE:
144 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
146 <220> FEATURE:
W--> 147 <221> NAME/KEY: Residue
148 <222> LOCATION: (1)
149 <223> OTHER INFORMATION: Xaa = Tyr, Arg, Phe, Gly, Trp, His or Asp
151 <220> FEATURE:
W--> 152 <221> NAME/KEY: Residue
153 <222> LOCATION: (2)
154 <223> OTHER INFORMATION: Xaa = Arg, Tyr, Trp, Ala, Val, Gln, His or Lys
156 <220> FEATURE:
W--> 157 <221> NAME/KEY: Residue
158 <222> LOCATION: (3)
159 <223> OTHER INFORMATION: Xaa = Lys, Tyr, Arg, Glu, Met or Trp
161 <220> FEATURE:
W--> 162 <221> NAME/KEY: Residue
163 <222> LOCATION: (4)
164 <223> OTHER INFORMATION: Xaa = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, Asn, Gln, His,
Lys, Arg,
165 Phe or Trp
167 <220> FEATURE:
W--> 168 <221> NAME/KEY: Residue
169 <222> LOCATION: (5)
170 <223> OTHER INFORMATION: Xaa = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, Asn, Gln, His,
Lys, Arg,
171 Phe, Tyr or Trp
W--> 173 <400> SEQUENCE: 4
W--> 174 Xaa Xaa Xaa Xaa Xaa
175 1 5
177 <210> SEQ ID NO: 5
178 <211> LENGTH: 5
179 <212> TYPE: PRT
180 <213> ORGANISM: Artificial Sequence
182 <220> FEATURE:
183 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
185 <220> FEATURE:

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/757,655

DATE: 02/21/2002
TIME: 11:38:41

Input Set : A:\FUJII SEQUENCE LISTING.txt
Output Set: N:\CRF3\02212002\I757655.raw

W--> 186 <221> NAME/KEY: Residue
187 <222> LOCATION: (1)
188 <223> OTHER INFORMATION: Xaa = Tyr, Arg, Phe, Gly, Trp, His or Asp, or polypeptide residue that an
189 arbitrary amino acid stood in the N-terminal side from this amino acid
191 <220> FEATURE:
W--> 192 <221> NAME/KEY: Residue
193 <222> LOCATION: (2)
194 <223> OTHER INFORMATION: Xaa = Arg, Tyr, Trp, Ala, Val, Gln, His or Lys
196 <220> FEATURE:
W--> 197 <221> NAME/KEY: Residue
198 <222> LOCATION: (3)
199 <223> OTHER INFORMATION: Xaa = Lys, Tyr, Arg, Glu, Met or Trp
201 <220> FEATURE:
W--> 202 <221> NAME/KEY: Residue
203 <222> LOCATION: (4)
204 <223> OTHER INFORMATION: Xaa = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, Asn, Gln, His, Lys, Arg,
205 Phe or Trp
207 <220> FEATURE:
W--> 208 <221> NAME/KEY: Residue
209 <222> LOCATION: (5)
210 <223> OTHER INFORMATION: Xaa = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, Asn, Gln, His, Lys, Arg,
211 Phe, Tyr or Trp
213 <400> SEQUENCE: 5
W--> 214 Xaa Xaa Xaa Xaa Xaa
215 1 5
217 <210> SEQ ID NO: 6
218 <211> LENGTH: 5
219 <212> TYPE: PRT
220 <213> ORGANISM: Artificial Sequence
222 <220> FEATURE:
223 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
225 <220> FEATURE:
W--> 226 <221> NAME/KEY: Residue
227 <222> LOCATION: (1)
228 <223> OTHER INFORMATION: Xaa = Tyr, Arg, Phe, Gly, Trp, His or Asp
230 <220> FEATURE:
W--> 231 <221> NAME/KEY: Residue
232 <222> LOCATION: (2)
233 <223> OTHER INFORMATION: Xaa = Arg, Tyr, Trp, Ala, Val, Gln, His or Lys
235 <220> FEATURE:
W--> 236 <221> NAME/KEY: Residue
237 <222> LOCATION: (3)
238 <223> OTHER INFORMATION: Xaa = Lys, Tyr, Arg, Glu, Met or Trp
240 <220> FEATURE:
W--> 241 <221> NAME/KEY: Residue
242 <222> LOCATION: (4)
243 <223> OTHER INFORMATION: Xaa = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, Asn, Gln, His, Lys, Arg,
244 Phe or Trp
246 <220> FEATURE:

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/757,655

DATE: 02/21/2002

TIME: 11:38:41

Input Set : A:\FUJII SEQUENCE LISTING.txt

Output Set: N:\CRF3\02212002\I757655.raw

W--> 247 <221> NAME/KEY: Residue
 248 <222> LOCATION: (5)
 249 <223> OTHER INFORMATION: Xaa = Gly, Ala, Val, Leu, Ile, Ser, Thr, Met, Asn, Gln, His,
 Lys, Arg,
 250 Phe, Tyr or Trp, or polypeptide residue that an arbitrary amino acid stood in
 line
 251 in the C-terminal side of this amino acid
 253 <400> SEQUENCE: 6/
 W--> 254 Xaa Xaa Xaa Xaa Xaa
 255 1 5
 257 <210> SEQ ID NO: 7
 258 <211> LENGTH: 7
 259 <212> TYPE: PRT
 260 <213> ORGANISM: Artificial Sequence
 262 <220> FEATURE:
 263 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
 265 <400> SEQUENCE: 7
 266 Gly Gly Asp Val Lys Ala Gly
 267 1 5
 269 <210> SEQ ID NO: 8
 270 <211> LENGTH: 6
 271 <212> TYPE: PRT
 272 <213> ORGANISM: Artificial Sequence
 274 <220> FEATURE:
 275 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
 277 <400> SEQUENCE: 8
 278 Gly Asp Val Lys Ala Gly
 279 1 5
 281 <210> SEQ ID NO: 9
 282 <211> LENGTH: 6
 283 <212> TYPE: PRT
 284 <213> ORGANISM: Artificial Sequence
 286 <220> FEATURE:
 287 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
 289 <400> SEQUENCE: 9
 290 Gly Tyr Tyr Lys Ala Ala
 291 1 5
 293 <210> SEQ ID NO: 10
 294 <211> LENGTH: 6
 295 <212> TYPE: PRT
 296 <213> ORGANISM: Artificial Sequence
 298 <220> FEATURE:
 299 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
 301 <400> SEQUENCE: 10
 302 Gly Tyr Ala Tyr Arg Lys
 303 1 5
 305 <210> SEQ ID NO: 11
 306 <211> LENGTH: 6
 307 <212> TYPE: PRT
 308 <213> ORGANISM: Artificial Sequence
 310 <220> FEATURE:

*Please correct
 this error in
 subsequent sequences*

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/757,655

DATE: 02/21/2002

TIME: 11:38:42

Input Set : A:\FUJII SEQUENCE LISTING.txt

Output Set: N:\CRF3\02212002\I757655.raw

L:30 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:35 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:40 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:45 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:50 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:56 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:68 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:74 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:79 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:84 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:89 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:95 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:107 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:112 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:117 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:122 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:127 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:134 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:147 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:152 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:157 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:162 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:168 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:174 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:186 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:192 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:197 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:202 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:208 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:226 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:231 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:236 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:241 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:247 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6